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## SEQUENCE LISTING

<110> THE CORPORATION OF THE TRUSTEES OF THE ORDER OF THE SISTERS OF  
MERCY IN QUEENSLAND

<120> NOVEL THERAPEUTIC MOLECULES AND USES THEREOF

<130> 12381870/TDO

<150> 2002953223

<151> 2002-06-12

<160> 32

<170> PatentIn version 3.1

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<222> (1)..(5619)

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Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
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Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His	
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aaa tgg aca gat aac aga gag	ctg acg tac agt aac	ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu	Leu Thr Tyr Ser Asn	Phe His Pro	
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Leu Leu Val Ser Gly Arg Leu	Arg Ile Pro Glu Asn	Phe Phe Glu	
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Glu Glu Ser Arg Tyr His Cys	Ala Leu Ile Leu Asn	Leu Gln Lys	
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Ser Pro Phe Thr Gly Thr Trp	Asn Phe Thr Ser Cys	Ser Glu Arg	
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His Phe Val Ser Leu Cys Gln	Lys Tyr Ser Glu Val	Lys Ser Arg	
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Gln Thr Leu Gln Asn Ala Ser	Glu Thr Val Lys Tyr	Leu Asn Asn	
1100	1105	1110	
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Leu Tyr Lys Ile Ile Pro Lys	Thr Leu Thr Trp His	Ser Ala Lys	
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Arg Glu Cys Leu Lys Ser Asn	Met Gln Leu Val Ser	Ile Thr Asp	
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Phe Gly Trp Ser Asp Gly Lys	Arg Leu His Phe Ser	Arg Trp Ala	
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Val Asp	Ser Val Lys Cys Pro	Ser Pro Val Leu Asn	Thr Pro Trp	
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ata cca	ttt cag aac tgt tgc	tac aat ttc ata ata	aca aag aat	3789
Ile Pro	Phe Gln Asn Cys Cys	Tyr Asn Phe Ile Ile	Thr Lys Asn	
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Arg His	Met Ala Thr Thr Gln	Asp Glu Val His Thr	Lys Cys Gln	
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Lys Leu	Asn Pro Lys Ser His	Ile Leu Ser Ile Arg	Asp Glu Lys	
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Thr Trp	Tyr Glu Ala Leu Asn	Met Cys Ser Gln Ser	Gly Gly His	
1415	1420	1425		

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Gln Ser Trp Ser Trp Leu Asp Gly Ser Glu Val Thr Phe Val Lys	
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser  
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His  
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His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly  
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His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly  
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Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp  
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Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro  
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Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile  
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Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu  
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Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp  
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Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser  
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Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile  
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Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly  
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Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro  
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Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met  
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Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu  
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Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp  
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Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn  
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Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys  
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Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr  
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Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr  
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Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu  
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Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn  
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Leu	Tyr	Lys	Ile	Ile	Pro	Lys	Thr	Leu	Thr	Trp	His	Ser	Ala	Lys
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Asp Ile	Leu Leu Gly Met	Phe	Tyr Asp Thr Asp Asp	Ala Ser Phe
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Lys Trp	Phe Asp Asn Ser	Asn	Met Thr Phe Asp Lys	Trp Thr Asp
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Gln Asp	Asp Asp Glu Asp	Leu	Val Asp Thr Cys Ala	Phe Leu His
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Ser Thr	Val Ile Leu Thr	Val	Leu Gly Ala Ile Ile	Trp Phe Leu
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cac gag gcc tcg cts gtg ctg ctg agc cta gcc act gyc atc ttc gct      48
His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala
1          5          10          15

gac tgt cct tcg tcc atc tgg gtt cag ttc caa ggc agc tgt tac act      96
Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
          20          25          30

ttt ctt caa gta acc atc aat gtg gaa aac ata gag gat gtc aga aag      144
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
          35          40          45

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cag tgt act gat cac ggg gca gac ctg gta agt ata cac aat gaa gaa Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu 50 55 60	192
gaa aac gca ttt ata ctg gac act tta caa aag cga tgg aaa ggc ccg Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro 65 70 75 80	240
gat gat ctt ctg cta ggc atg ttt tat gac act gat gat gca agt ttc Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe 85 90 95	288
aag tgg ttt gat cag tca aat atg aca ttc gac aag tgg gca gat gag Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu 100 105 110	336
gat ggt gag gac cta gtt gac acc tgt ggt ttt ctg tat gcc aag aca Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr 115 120 125	384
ggt gaa tgg aga aaa gga aat tgt gaa atg tct tct gtg acr gga aca Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr 130 135 140	432
ctt tgc aaa aca gca atc cca tat gac aag aag tat tta tca gat aac Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn 145 150 155 160	480
cac att tta ata tcg act ctg gtg atc gct agc aca gtg act ctg gca His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala 165 170 175	528
gtt ttg gga gcg gtc att tgg ttc ctc tat aga agg agc gca cgc tct Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser 180 185 190	576
ggc ttc acc tct ttc tct cct gca cca caa tca cct tac agt gat ggc Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly 195 200 205	624
tgt gct ctg gta gtt gcg gaa gaa gat gaa tac tct gtt cag ctg gac Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp 210 215 220	672
tgagagtttg ggaacatcag acgagcacac tgaacacctt gacaagaaat aatttcctat	732
gcaagatttgt catgtaaaaat ttgccacgga aaactgaacc ttttatggta ttccttattc	792
ttctaacaat attttcatgt attcaatgtg acaaaacata aaccttctga ttaaaaggaa	852
aaaaagtagg tttcagaaaa ggaactagca cagagctaac ttacagggtt tcttaagtag	912
ttttcatttg agtaaatgaa agctacagta caataaagct ggtaaaacgc aaaaaaaaaa	972
aaaaaaa	979

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<210> 11  
 <211> 224  
 <212> PRT  
 <213> mammalian

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> The 'Xaa' at location 5 stands for Leu.

<220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> The 'Xaa' at location 13 stands for Ala, or Val.

<220>  
 <221> misc\_feature  
 <222> (142)..(142)  
 <223> The 'Xaa' at location 142 stands for Thr.

<400> 11

His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala  
 1 5 10 15

Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr  
 20 25 30

Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys  
 35 40 45

Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu  
 50 55 60

Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro  
 65 70 75 80

Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe  
 85 90 95

Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu  
 100 105 110

Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr  
 115 120 125

Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr  
 130 135 140

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Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn  
 145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala  
 165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser  
 180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly  
 195 200 205

Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp  
 210 215 220

<210> 12  
 <211> 979  
 <212> DNA  
 <213> mammalian

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 aggtagaccc aagtcaaggt tccgtcgaca atgtgaaaag aagttcattg gtagttacac 120  
 cttttgtatc tcctacagtc tttcgtcaca tgactagtgc cccgtctgga ccattcatat 180  
 gtgttacttc ttcttttgog taaatatgac ctgtgaaatg ttttcgctac ctttcggggc 240  
 ctactagaag acgatccgta caaaatactg tgactactac gttcaaagtt caccaaacta 300  
 gtcagtttat actgtaagct gttcaccogt ctactcctac cactcctgga tcaactgtgg 360  
 acaccaaaaag acatacgggt ctgtccactt acctcttttc ctttaacact ttacagaaga 420  
 cactgycctt gtgaaacggt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480  
 gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540  
 cagtaaacca aggagatata ttcctcgcgt gcgagaccga agtggagaaa gagaggacgt 600  
 ggtgttagtg gaatgtcact accgacacga gaccatcaac gccttcttct acttatgaga 660  
 caagtcgacc tgactctcaa accctttag tagtctcgtg tgacttgtgg aactgttctt 720  
 tattaaagga tacgttctaa cagtacattt taaacggtgc cttttgactt ggaaaatacc 780  
 ataaggaata agaagattgt tataaaagta cataagttac actgttttgt atttggaaga 840  
 ctaattttcc tttttttcat ccaaagtctt ttccttgatc gtgtctcgat tgaatgtcca 900

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aaagaattca tcaaaagtaa actcattttac ttctgatgtc atgttatttc gaccattttg 960  
cgtttttttt ttttttttt 979

<210> 13  
<211> 483  
<212> DNA  
<213> mammalian  
  
<220>  
<221> misc\_feature  
<222> (43)..(43)  
<223> n is any nucleic acid

<400> 13  
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ctgtgaagtt tcttctgtgg aaggaaccct ttgtaaagca gctatcccat atgaaaagaa 120  
atatttatca gataaccgca ttttaatatc agctttgggtg attgctagca cagtaattct 180  
gacagttctg ggagcagttg ttgggttctt gtacaaaaga agtttggatt ctggtttcac 240  
cacagttttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300  
agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360  
aatacctttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaaattagt 420  
ttttatgata tattacctta ttccagtaac attcattact cttatgtaaa atcactgatc 480  
atg 483

<210> 14  
<211> 27  
<212> DNA  
<213> mammalian

<220>  
<221> CDS  
<222> (1)..(27)  
<223>

<400> 14  
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Lys Val Pro Leu Gly Pro Asp Tyr Thr  
1 5

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<210> 15  
 <211> 9  
 <212> PRT  
 <213> mammalian

<400> 15

Lys Val Pro Leu Gly Pro Asp Tyr Thr  
 1 5

<210> 16  
 <211> 42  
 <212> DNA  
 <213> mammalian

<220>  
 <221> CDS  
 <222> (1)..(42)  
 <223>

<400> 16  
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 Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe 42  
 1 5 10

<210> 17  
 <211> 14  
 <212> PRT  
 <213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe  
 1 5 10

<210> 18  
 <211> 42  
 <212> DNA  
 <213> mammalian

<220>  
 <221> CDS  
 <222> (1)..(42)  
 <223>

<400> 18  
 gct gcc gtc gcg gac tgt cct tca tct act tgg att cag ttc  
 Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe 42  
 1 5 10

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<210> 19  
 <211> 14  
 <212> PRT  
 <213> mammalian

<400> 19

Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe  
 1 5 10

<210> 20  
 <211> 5454  
 <212> DNA  
 <213> mammalian  
 <220>  
 <221> CDS  
 <222> (1)..(5451)  
 <223>

<400> 20

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Met Arg Thr Gly Trp Ala Thr Pro Arg Arg Pro Ala Gly Leu Leu Met	
1 5 10 15	
ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct	96
Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
20 25 30	
aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag	144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
35 40 45	
cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac	192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
50 55 60	
aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc	240
Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
65 70 75 80	
caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga	288
Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	
85 90 95	
atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac	336
Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His	
100 105 110	
cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga	384
His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly	
115 120 125	

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cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly 130 135 140	432
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg 145 150 155 160	480
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp 165 170 175	528
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro 180 185 190	576
tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile 195 200 205	624
tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu 210 215 220	672
cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp 225 230 235 240	720
aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser 245 250 255	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile 260 265 270	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly 275 280 285	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro 290 295 300	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met 305 310 315 320	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu 325 330 335	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp 340 345 350	1056

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gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn 355 360 365	1104
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys 370 375 380	1152
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His 385 390 395 400	1200
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp 405 410 415	1248
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr 420 425 430	1296
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp 435 440 445	1344
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser 450 455 460	1392
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys 465 470 475 480	1440
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser 485 490 495	1488
tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu 500 505 510	1536
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys 515 520 525	1584
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu 530 535 540	1632
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu 545 550 555 560	1680
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly 565 570 575	1728



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aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776
Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala	
580 585 590	
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag	1824
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys	
595 600 605	
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872
Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys	
610 615 620	
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat	1920
Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp	
625 630 635 640	
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt	1968
Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys	
645 650 655	
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa	2016
Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu	
660 665 670	
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc	2064
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe	
675 680 685	
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag	2112
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln	
690 695 700	
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca	2160
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro	
705 710 715 720	
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act	2208
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr	
725 730 735	
att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt	2256
Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys	
740 745 750	
gct gct gtc aag gta ttt cat agg cca tgg cga aga ggc tgg cat ttc	2304
Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe	
755 760 765	
tat gat gat aga gaa ttt att tat ttg agg cct ttt gct tgt gat aca	2352
Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr	
770 775 780	
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca	2400
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr	
785 790 795 800	

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cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu 805 810 815	2448
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn 820 825 830	2496
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala 835 840 845	2544
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala 850 855 860	2592
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp 865 870 875 880	2640
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe 885 890 895	2688
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp 900 905 910	2736
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe 915 920 925	2784
atc tgt gaa aaa tat aat gtt tot tgc tta gag aaa tac agc cca gat Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp 930 935 940	2832
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn 945 950 955 960	2880
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala 965 970 975	2928
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser 980 985 990	2976
cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala 995 1000 1005	3024
act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn 1010 1015 1020	3069

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aaa tgg Lys Trp 1025	aca gat Thr Asp	aac aga Asn Arg	gag Glu 1030	ctg acg Leu Thr	tac agt Tyr Ser	aac Asn 1035	ttt cac Phe His	cca Pro	3114
tta ttg Leu Leu 1040	gtt agt Val Ser	ggg agg Gly Arg	ctg Leu 1045	aga ata Arg Ile	cca gaa Pro Glu	aat Asn 1050	ttt ttt Phe Phe	gag Glu	3159
gaa gag Glu Glu 1055	tct cgc Ser Arg	tac cac Tyr His	tgt Cys 1060	gcc cta Ala Leu	ata ctc Ile Leu	aac Asn 1065	ctc caa Leu Gln	aaa Lys	3204
tca ccg Ser Pro 1070	ttt act Phe Thr	ggg acg Gly Thr	tgg Trp 1075	aat ttt Asn Phe	aca tcc Thr Ser	tgc Cys 1080	agt gaa Ser Glu	cgc Arg	3249
cac ttt His Phe 1085	gtg tct Val Ser	ctc tgt Leu Cys	cag Gln 1090	aaa tat Lys Tyr	tca gaa Ser Glu	gtt Val 1095	aaa agc Lys Ser	aga Arg	3294
cag acg Gln Thr 1100	ttg cag Leu Gln	aat gct Asn Ala	tca Ser 1105	gaa act Glu Thr	gta aag Val Lys	tat Tyr 1110	cta aat Leu Asn	aat Asn	3339
ctg tac Leu Tyr 1115	aaa ata Lys Ile	atc cca Ile Pro	aag Lys 1120	act ctg Thr Leu	act tgg Thr Trp	cac His 1125	agt gct Ser Ala	aaa Lys	3384
agg gag Arg Glu 1130	tgt ctg Cys Leu	aaa agt Lys Ser	aac Asn 1135	atg cag Met Gln	ctg gtg Leu Val	agc Ser 1140	atc acg Ile Thr	gac Asp	3429
cct tac Pro Tyr 1145	cag cag Gln Gln	gca ttc Ala Phe	ctc Leu 1150	agt gtg Ser Val	cag gcg Gln Ala	ctc Leu 1155	ctt cac Leu His	aac Asn	3474
tct tcc Ser Ser 1160	tta tgg Leu Trp	atc gga Ile Gly	ctc Leu 1165	ttc agt Phe Ser	caa gat Gln Asp	gat Asp 1170	gaa ctc Glu Leu	aac Asn	3519
ttt ggt Phe Gly 1175	tgg tca Trp Ser	gat ggg Asp Gly	aaa Lys 1180	cgt ctt Arg Leu	cat ttt His Phe	agt Ser 1185	cgc tgg Arg Trp	gct Ala	3564
gaa act Glu Thr 1190	aat ggg Asn Gly	caa ctc Gln Leu	gaa Glu 1195	gac tgt Asp Cys	gta gta Val Val	tta Leu 1200	gac act Asp Thr	gat Asp	3609
gga ttc Gly Phe 1205	tgg aaa Trp Lys	aca gtt Thr Val	gat Asp 1210	tgc aat Cys Asn	gac aat Asp Asn	caa Gln 1215	cca ggt Pro Gly	gct Ala	3654
att tgc Ile Cys 1220	tac tat Tyr Tyr	tca gga Ser Gly	aat Asn 1225	gag act Glu Thr	gaa aaa Glu Lys	gag Glu 1230	gtc aaa Val Lys	cca Pro	3699

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gtt gac agt gtt aaa tgt cca tct cct gtt cta aat act ccg tgg	3744
Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp	
1235 1240 1245	
ata cca ttt cag aac tgt tgc tac aat ttc ata ata aca aag aat	3789
Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn	
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agg cat atg gca aca aca cag gat gaa gtt cat act aaa tgc cag	3834
Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln	
1265 1270 1275	
aaa ctg aat cca aaa tca cat att ctg agt att cga gat gaa aag	3879
Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys	
1280 1285 1290	
gag aat aac ttt gtt ctt gag caa ctg ctg tac ttc aat tat atg	3924
Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met	
1295 1300 1305	
gct tca tgg gtc atg tta gga ata act tat aga aat aat tct ctt	3969
Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu	
1310 1315 1320	
atg tgg ttt gat aag acc cca ctg tca tat aca cat tgg aga gca	4014
Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala	
1325 1330 1335	
gga aga cca act ata aaa aat gag aag ttt ttg gct ggt tta agt	4059
Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser	
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act gac ggc ttc tgg gat att caa acc ttt aaa gtt att gaa gaa	4104
Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu	
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gca gtt tat ttt cac cag cac agc att ctt gct tgt aaa att gaa	4149
Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu	
1370 1375 1380	
atg gtt gac tac aaa gaa gaa cat aat act aca ctg cca cag ttt	4194
Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe	
1385 1390 1395	
atg cca tat gaa gat ggt att tac agt gtt att caa aaa aag gta	4239
Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val	
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aca tgg tat gaa gca tta aac atg tgt tct caa agt gga ggt cac	4284
Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His	
1415 1420 1425	
ttg gca agc gtt cac aac caa aat ggc cag ctc ttt ctg gaa gat	4329
Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp	
1430 1435 1440	

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att gta aaa cgt gat gga ttt cca cta tgg gtt ggg ctc tca agt Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu Ser Ser 1445 1450 1455	4374
cat gat gga agt gaa tca agt ttt gaa tgg tct gat ggt agt aca His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr 1460 1465 1470	4419
ttt gac tat atc cca tgg aaa ggc caa aca tct cct gga aat tgt Phe Asp Tyr Ile Pro Trp Lys Gly Gln Thr Ser Pro Gly Asn Cys 1475 1480 1485	4464
gtt ctc ttg gat cca aaa gga act tgg aaa cat gaa aaa tgc aac Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn 1490 1495 1500	4509
tct gtt aag gat ggt gct att tgt tat aaa cct aca aaa tct aaa Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Ser Lys 1505 1510 1515	4554
aag ctg tcc cgt ctt aca tat tca tca aga tgt cca gca gca aaa Lys Leu Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys 1520 1525 1530	4599
gag aat ggg tca cgg tgg atc cag tac aag ggt cac tgt tac aag Glu Asn Gly Ser Arg Trp Ile Gln Tyr Lys Gly His Cys Tyr Lys 1535 1540 1545	4644
tct gat cag gca ttg cac agt ttt tca gag gcc aaa aaa ttg tgt Ser Asp Gln Ala Leu His Ser Phe Ser Glu Ala Lys Lys Leu Cys 1550 1555 1560	4689
tca aaa cat gat cac tct gca act atc gtt tcc ata aaa gat gaa Ser Lys His Asp His Ser Ala Thr Ile Val Ser Ile Lys Asp Glu 1565 1570 1575	4734
gat gag aat aaa ttt gtg agc aga ctg atg agg gaa aat aat aac Asp Glu Asn Lys Phe Val Ser Arg Leu Met Arg Glu Asn Asn Asn 1580 1585 1590	4779
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ttt ctc caa gaa gcc atc aaa gta gaa agc ata gag gat gtc aga Phe Leu Gln Glu Ala Ile Lys Val Glu Ser Ile Glu Asp Val Arg 1625 1630 1635	4914
aat cag tgt act gac cat gga gcg gac atg ata agc ata cat aat Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile Ser Ile His Asn 1640 1645 1650	4959

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gaa gaa gaa aat gct ttt ata ctg gat act ttg aaa aag caa tgg	5004
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aaa ggc cca gat gat atc cta cta ggc atg ttt tat gac aca gat	5049
Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp Thr Asp	
1670 1675 1680	
gat gcg agt ttc aag tgg ttt gat aat tca aat atg aca ttt gat	5094
Asp Ala Ser Phe Lys Trp Phe Asp Asn Ser Asn Met Thr Phe Asp	
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aag tgg aca gac caa gat gat gat gag gat tta gtt gac acc tgt	5139
Lys Trp Thr Asp Gln Asp Asp Asp Glu Asp Leu Val Asp Thr Cys	
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gct ttt ctg cac atc aag aca ggt gaa tgg aaa aaa gga aat tgt	5184
Ala Phe Leu His Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys	
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gaa gtt tct tct gtg gaa gga aca cta tgc aaa aca gct atc cca	5229
Glu Val Ser Ser Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro	
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tac aaa agg aaa tat tta tca gat aac cac att tta ata tca gca	5274
Tyr Lys Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala	
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ttg gtg att gct agc acg gta att ttg aca gtt ttg gga gca atc	5319
Leu Val Ile Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile	
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Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr	
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Val Phe Ser Thr Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val	
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Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys  
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Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp  
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Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser  
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Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg  
 85 90 95

Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His  
 100 105 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly  
 115 120 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly  
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Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg  
 145 150 155 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp  
 165 170 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro  
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Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile  
 195 200 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu  
 210 215 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp  
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Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser  
245 250 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile  
260 265 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly  
275 280 285

Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro  
290 295 300

Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met  
305 310 315 320

Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu  
325 330 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp  
340 345 350

Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn  
355 360 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys  
370 375 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His  
385 390 395 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp  
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr  
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp  
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser  
450 455 460



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Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys  
 465 470 475 480

Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser  
 485 490 495

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu  
 500 505 510

Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys  
 515 520 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu  
 530 535 540

Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu  
 545 550 555 560

Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly  
 565 570 575

Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala  
 580 585 590

Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys  
 595 600 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys  
 610 615 620

Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp  
 625 630 635 640

Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys  
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Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu  
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Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe  
 675 680 685

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Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln  
 690 695 700

Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro  
 705 710 715 720

Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr  
 725 730 735

Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys  
 740 745 750

Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe  
 755 760 765

Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr  
 770 775 780

Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr  
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Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu  
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Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn  
 820 825 830

Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala  
 835 840 845

Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala  
 850 855 860

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp  
 865 870 875 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe  
 885 890 895

Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp  
 900 905 910

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Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe  
           915                                  920                                  925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp  
           930                                  935                                  940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn  
   945                                  950                                  955                                  960

Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala  
                                   965                                  970                                  975

Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser  
                   980                                  985                                  990

Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala  
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Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn  
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Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro  
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Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu  
   1040                                  1045                                  1050

Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys  
   1055                                  1060                                  1065

Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg  
   1070                                  1075                                  1080

His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg  
   1085                                  1090                                  1095

Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn  
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Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys  
   1115                                  1120                                  1125

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Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp  
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Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn  
 1145 1150 1155

Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn  
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Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala  
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Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp  
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Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala  
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Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro  
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Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp  
 1235 1240 1245

Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn  
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Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln  
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Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys  
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Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met  
 1295 1300 1305

Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu  
 1310 1315 1320

Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala  
 1325 1330 1335

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Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser  
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Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu  
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Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu  
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Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe  
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Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val  
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Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His  
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Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp  
 1430 1435 1440

Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu Ser Ser  
 1445 1450 1455

His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly Ser Thr  
 1460 1465 1470

Phe Asp Tyr Ile Pro Trp Lys Gly Gln Thr Ser Pro Gly Asn Cys  
 1475 1480 1485

Val Leu Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn  
 1490 1495 1500

Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Ser Lys  
 1505 1510 1515

Lys Leu Ser Arg Leu Thr Tyr Ser Ser Arg Cys Pro Ala Ala Lys  
 1520 1525 1530

Glu Asn Gly Ser Arg Trp Ile Gln Tyr Lys Gly His Cys Tyr Lys  
 1535 1540 1545

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Ser	Asp	Gln	Ala	Leu	His	Ser	Phe	Ser	Glu	Ala	Lys	Lys	Leu	Cys
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Ser	Lys	His	Asp	His	Ser	Ala	Thr	Ile	Val	Ser	Ile	Lys	Asp	Glu
1565						1570					1575			
Asp	Glu	Asn	Lys	Phe	Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Asn	Asn
1580						1585					1590			
Ile	Thr	Met	Arg	Val	Trp	Leu	Gly	Leu	Ser	Gln	His	Ser	Val	Asp
1595						1600					1605			
Cys	Pro	Ser	Ser	Thr	Trp	Ile	Gln	Phe	Gln	Asp	Ser	Cys	Tyr	Ile
1610						1615					1620			
Phe	Leu	Gln	Glu	Ala	Ile	Lys	Val	Glu	Ser	Ile	Glu	Asp	Val	Arg
1625						1630					1635			
Asn	Gln	Cys	Thr	Asp	His	Gly	Ala	Asp	Met	Ile	Ser	Ile	His	Asn
1640						1645					1650			
Glu	Glu	Glu	Asn	Ala	Phe	Ile	Leu	Asp	Thr	Leu	Lys	Lys	Gln	Trp
1655						1660					1665			
Lys	Gly	Pro	Asp	Asp	Ile	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr	Asp
1670						1675					1680			
Asp	Ala	Ser	Phe	Lys	Trp	Phe	Asp	Asn	Ser	Asn	Met	Thr	Phe	Asp
1685						1690					1695			
Lys	Trp	Thr	Asp	Gln	Asp	Asp	Asp	Glu	Asp	Leu	Val	Asp	Thr	Cys
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Ala	Phe	Leu	His	Ile	Lys	Thr	Gly	Glu	Trp	Lys	Lys	Gly	Asn	Cys
1715						1720					1725			
Glu	Val	Ser	Ser	Val	Glu	Gly	Thr	Leu	Cys	Lys	Thr	Ala	Ile	Pro
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Tyr	Lys	Arg	Lys	Tyr	Leu	Ser	Asp	Asn	His	Ile	Leu	Ile	Ser	Ala
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Leu Val Ile Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile  
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Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr  
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